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5D5 Light Chain

```

1  AspIleMetMetSerGlnSerProSerSerLeuThrValSerValGlyGluLysValThrValSerCysLys
1  GACATTATGATGTCCAGTCTCCATCCTCCCTAACTGTCTCAGTTGGAGAGAGGTTACTGTGAGCTGCAAG
25 SerSerGlnSerLeuLeuTyrThrSerSerGlnLysAsnTyrLeuAlaTrpTyrGlnGlnLysProGlyGln
73 TCCAGTCAGTCCCTTTTATATACTAGCAGTCAGACAGAACTACTTGGCTGGTACCAGCAGAAACCAGGTGAG
49 SerProLysLeuLeuIleTyrTrpAlaSerThrArgGluSerGlyValProAspArgPheThrGlySerGly
145 TCTCCTAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGA
73 SerGlyThrAspPheThrLeuThrIleThrSerValLysAlaAspAspLeuAlaValTyrTyrCysGlnGln
217 TCTGGGACAGATTTCACTCTCACCATCACAGTGTGAAGCTGACGACCTGGCAGTTTATTACTGTACAGCAA
97 TyrTyrAlaTyrProTrpThrPheGlyGlyGlyThrLysLeuGluIleLysArgThrValAlaAlaProSer
289 TATTATGCCCTATCCGTGGACGTTCCGTGGAGGCACAAAGTTGGAGATCAACCGACCCGTGGCTGCACCATCT
121 ValPheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsn
361 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCTGCTGAATAAC
145 PheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSer
433 TTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCGGAGAGT
169 ValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyr
505 GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAGCAGACTAC
193 GluLysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsn
577 GAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTGCCCGCTCACAAACAGCTTCAAC
217 ArgGlyGluCys
649 AGGGGAGAGTGT

```

FIG. 1A

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505 Heavy Chain

1 GlxValGlnLeuGlnInserGlyProGluLeuValArgProGlyAlaSerValLysMetSerCysArgAla
1 SAGGTTCAAGCTGCAGCAGTCTGGGCCTGAACCTGGTGAGGCCTGGGGCTTCAGTGAAATGTCTCGAGGGCT
25 SerGlyTyrThrPheThrSerTyrTrpLeuHisTrpValLysGlnArgProGlyProGlyLeuGluTrpIle
73 TCGGGCTATACCTTCACCAAGCTACTGGTTGCACTGGGTAAACAGAGGCCTGGACCAGGCCTTGAGTGGATT
49 GlyMetIleAspProSerAsnSerAspThrArgPheAsnProAsnPheLysAspLysAlaThrLeuAsnVal
145 GGCATGATTGATCCCTTCCAATAGTGACACTAGGTTTAA TCCGAACITCAAGGACAAGGCCACATTGAATGTA
73 AspArgSerSerAsnThrAlaTyrMetLeuLeuSerSerLeuThrSerAlaAspSerAlaValTyrTyrCys
217 GACAGATCTTCCAAACACAGCCCTACATGCTGCTCAGCAGCCTGACATCTGCTGACTCTGCAGTCTATTACTGT
97 AlaThrTyrGlySerTyrValSerProLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAla
289 GCCACATATGGTAGCTACGTTTCCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTTCCGCC
121 SerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeu
361 TCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
145 GlyCysLeuValLysAspTyrPheProGluProValThrValSerTyrPheAsnSerGlyAlaLeuThrSerGly
433 GGCTGCCCTGGTCAAGGACTACTTCCCGAACCCTGACGGTGTCTGTGGAACCTCAGGGCGCCCTGACCAGCGGC
169 ValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSer
505 GTGCACACCTTCCCGGCTGTCTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCCTCC
193 SerSerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys
577 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACCAAGGTCGACAAAGAAA
217 ValGluProLysSerCysAspLysThrHisThrAlaAlaPro
649 GTTGAGCCCCAAATCTTGTGACAAACTCACACAGCTGGCGCCG

FIG. 1B

SUBSTITUTE SHEET (RULE 26)

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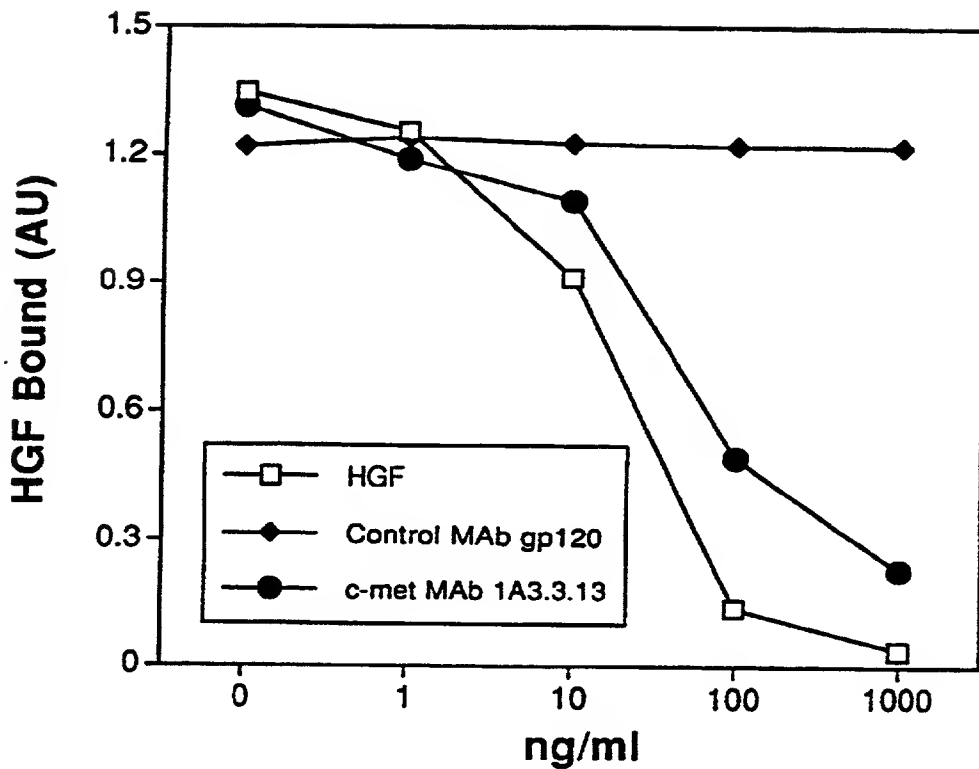


FIG. 2

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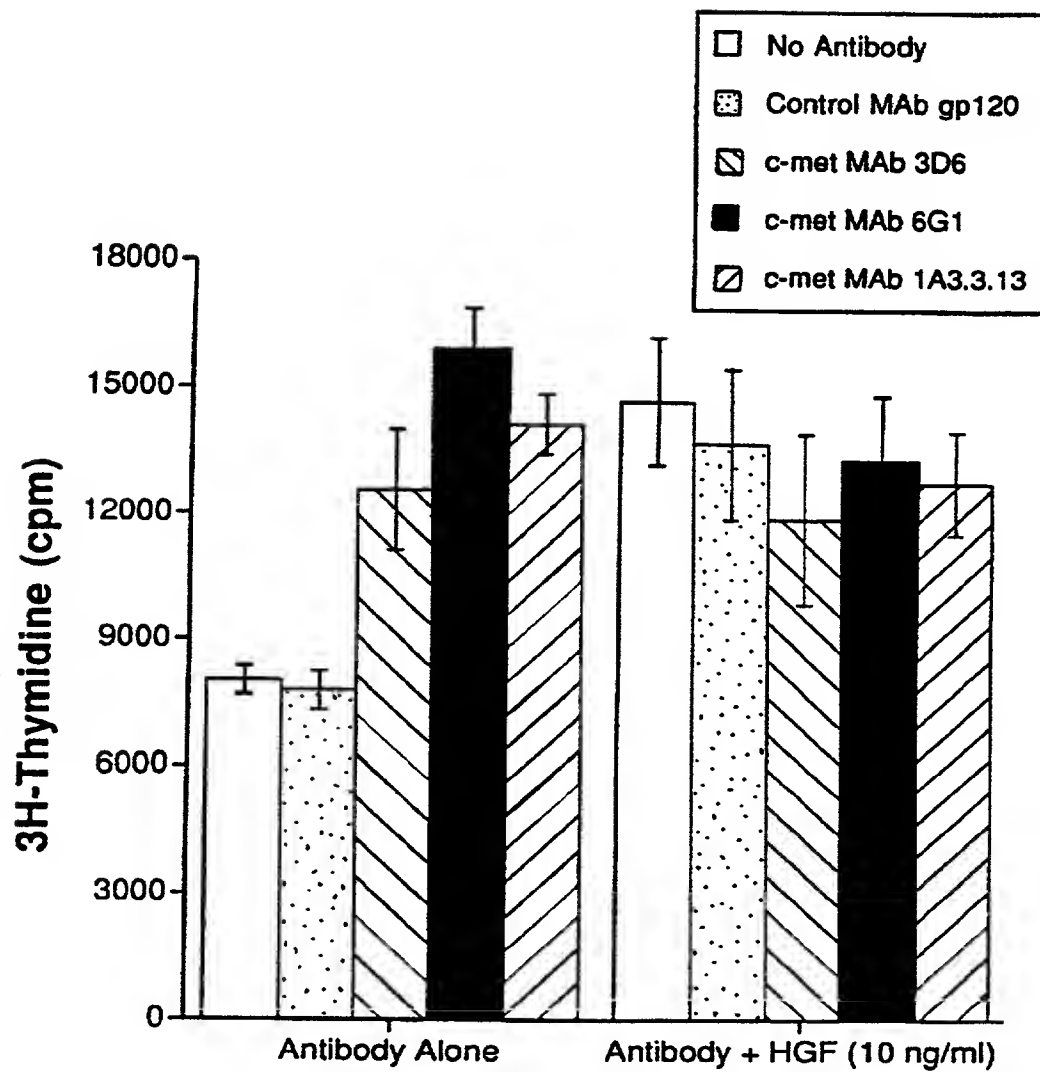


FIG. 3

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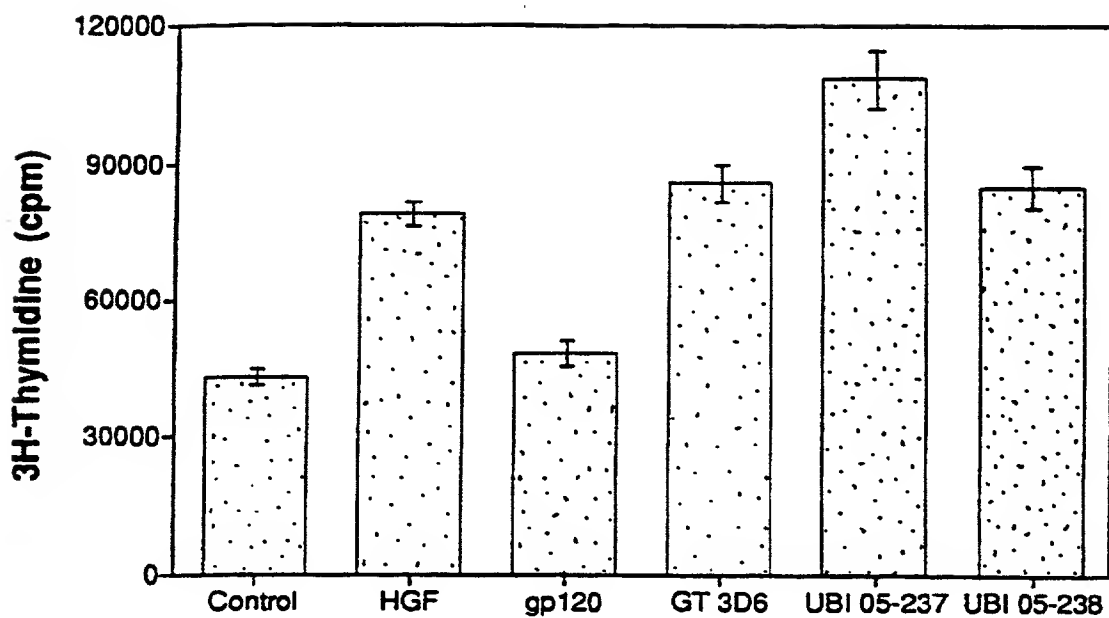


FIG. 4

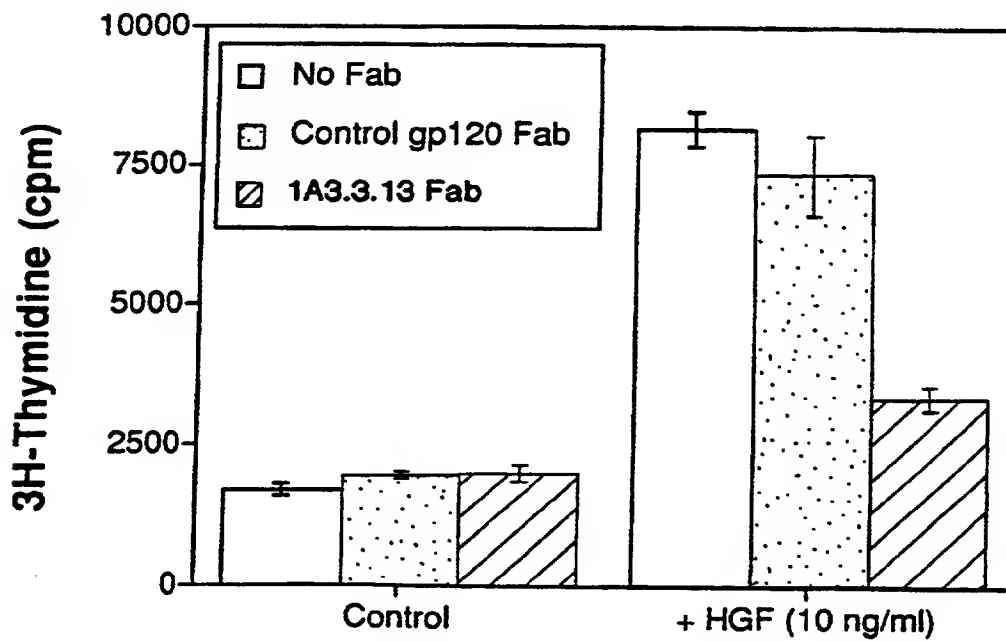
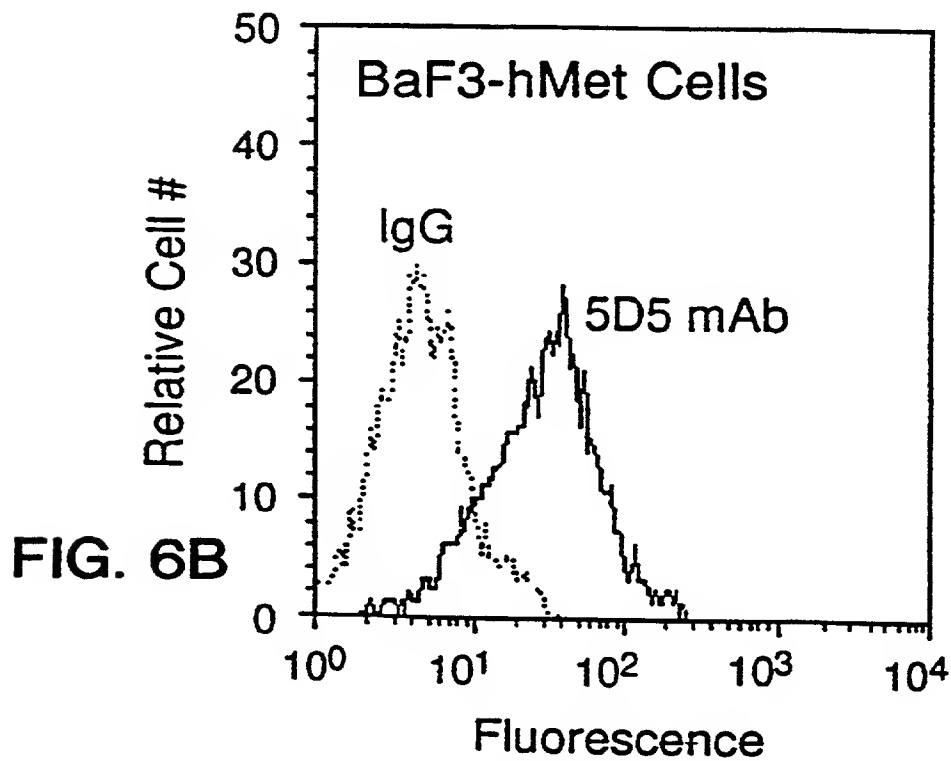
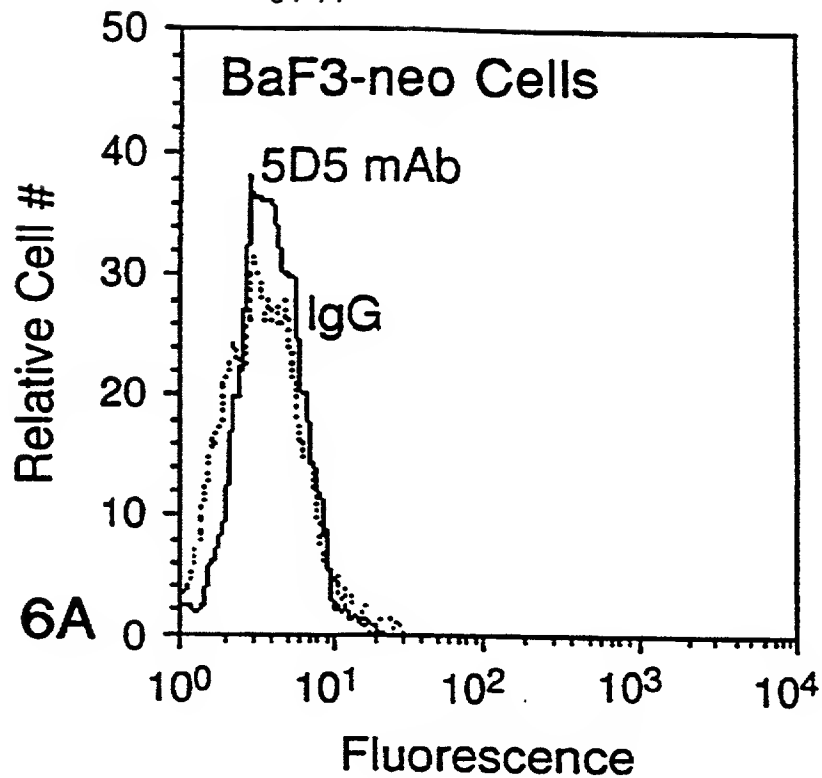


FIG. 5

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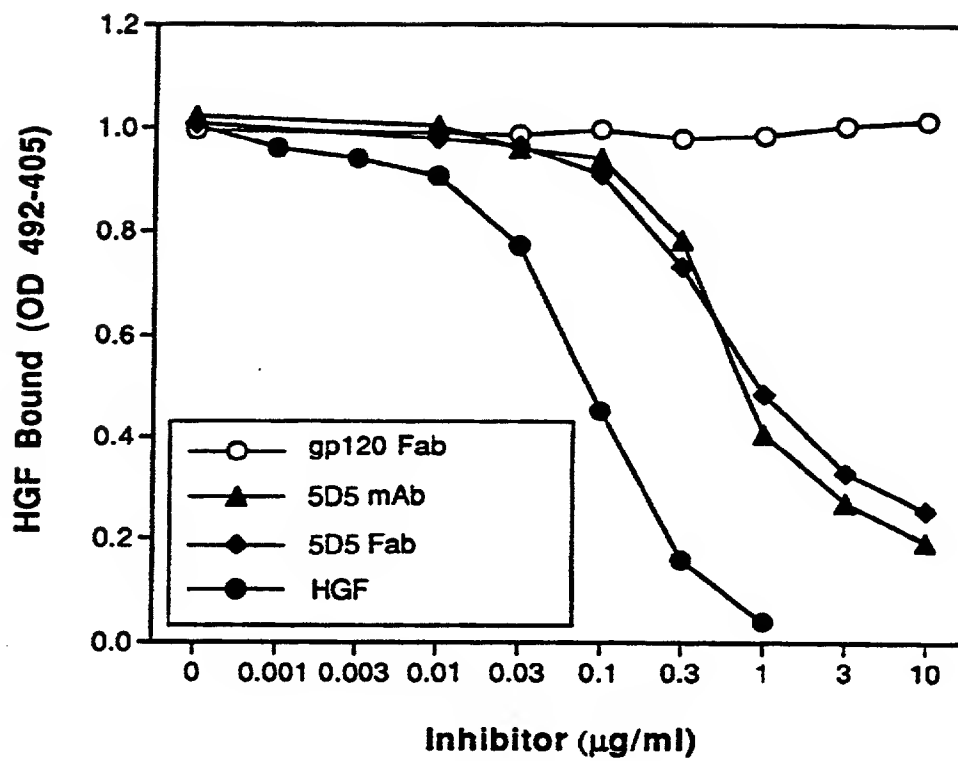


FIG. 7

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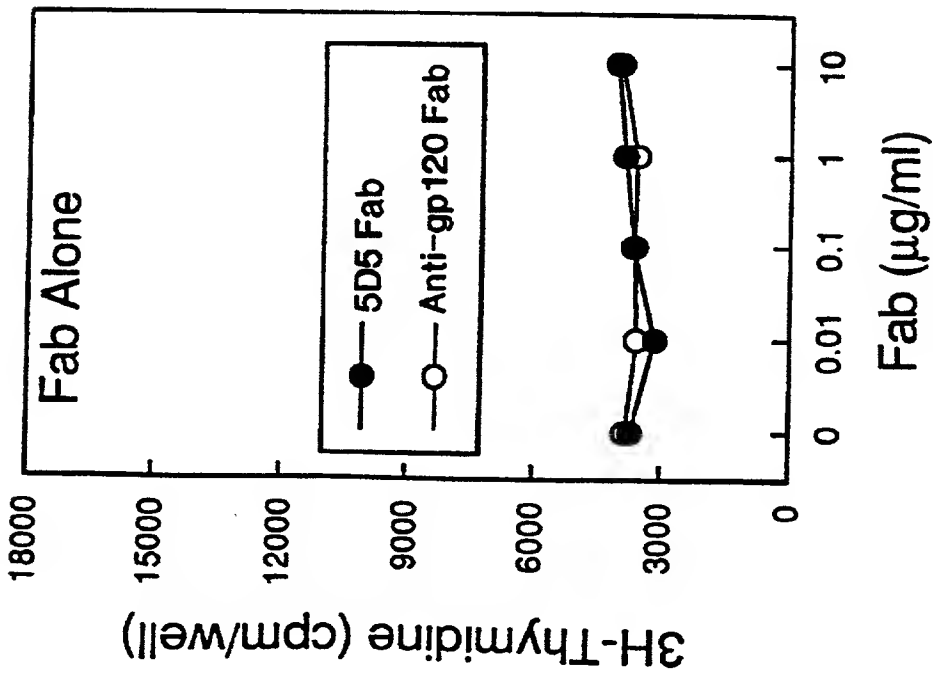


FIG. 8A

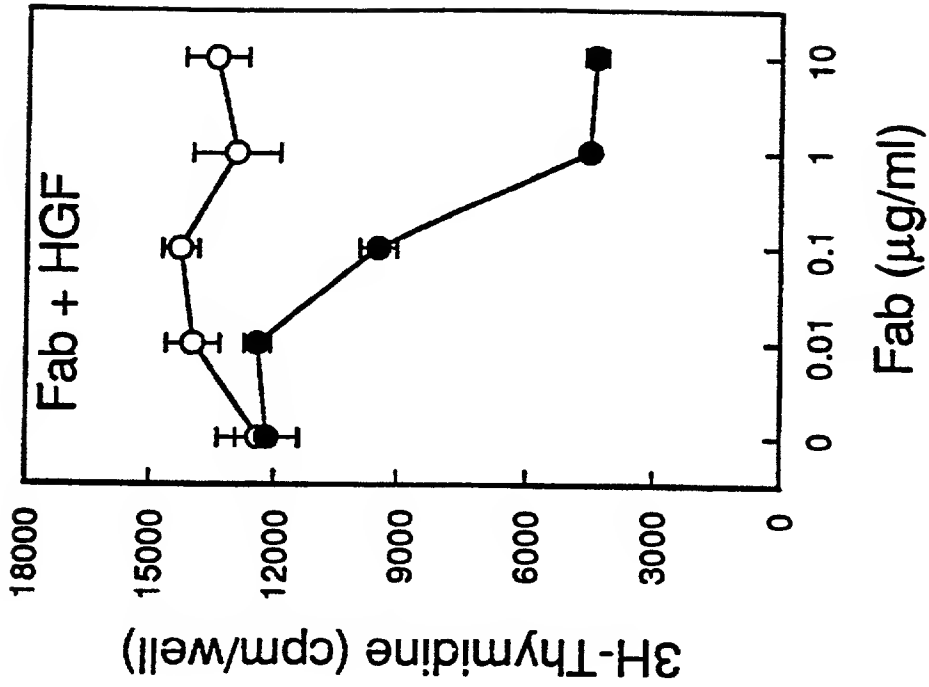


FIG. 8B

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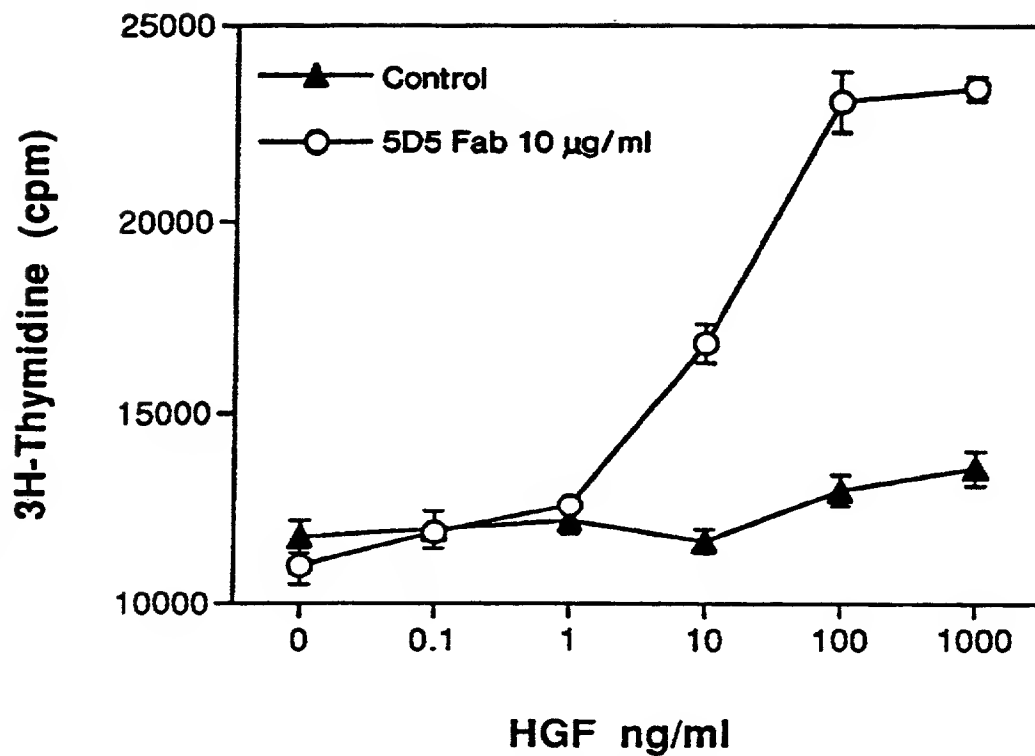
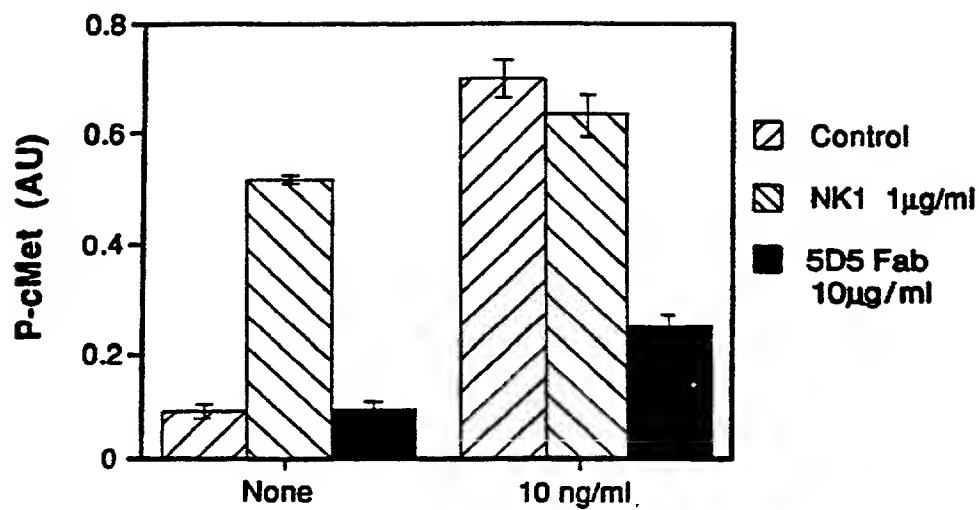


FIG. 9

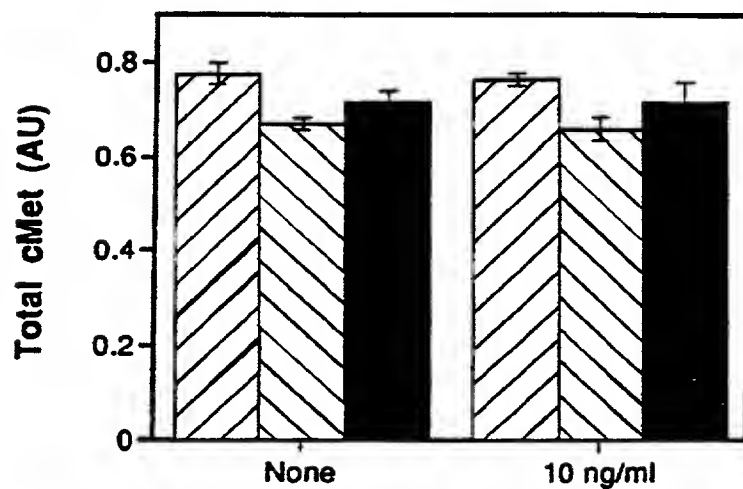
SUBSTITUTE SHEET (RULE 26)

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HGF

FIG. 10A



HGF

FIG. 10B

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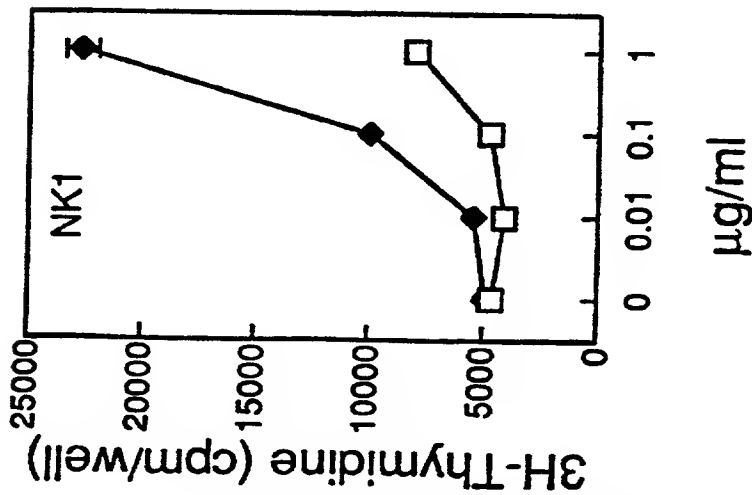


FIG. 11A

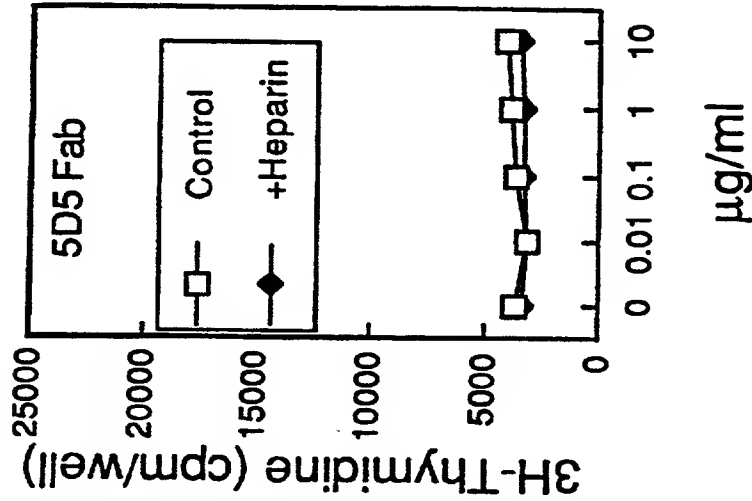


FIG. 11B

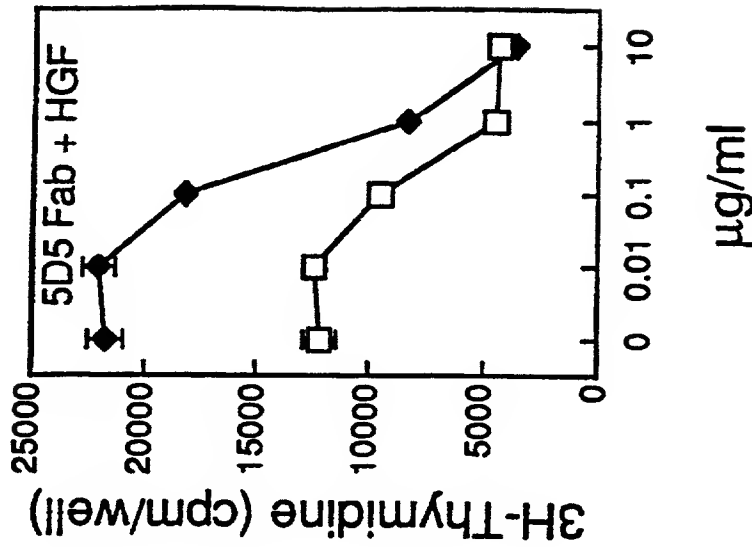
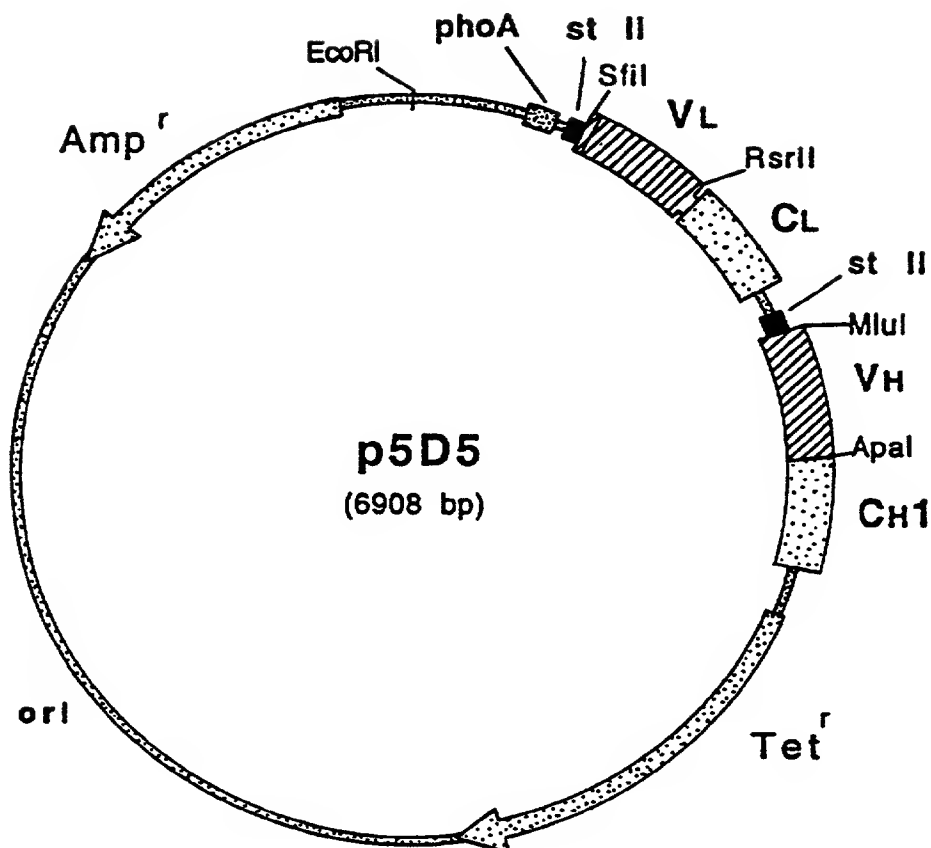


FIG. 11C

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**FIG. 12****SUBSTITUTE SHEET (RULE 26)**

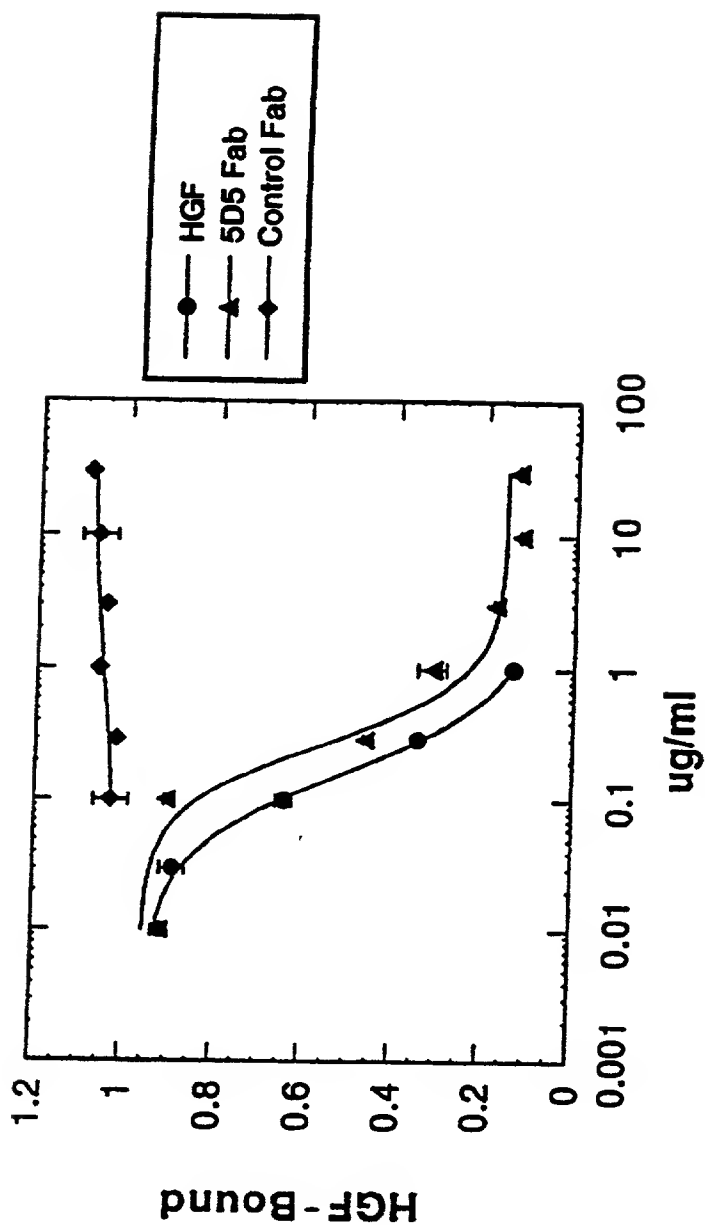


FIG. 13

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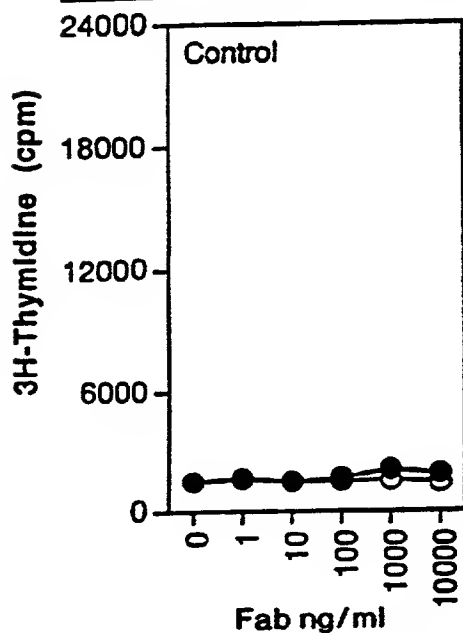
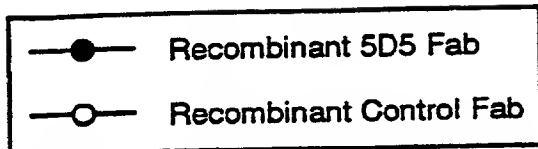


FIG. 14A

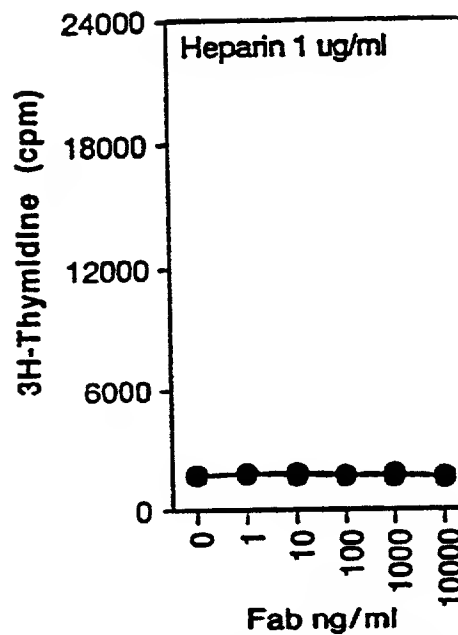


FIG. 14B

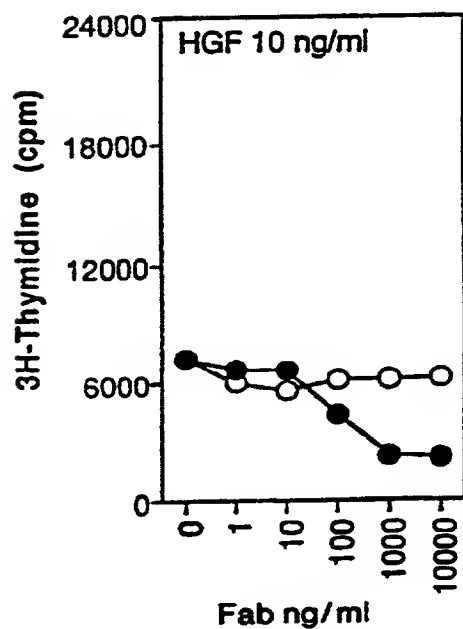


FIG. 14C

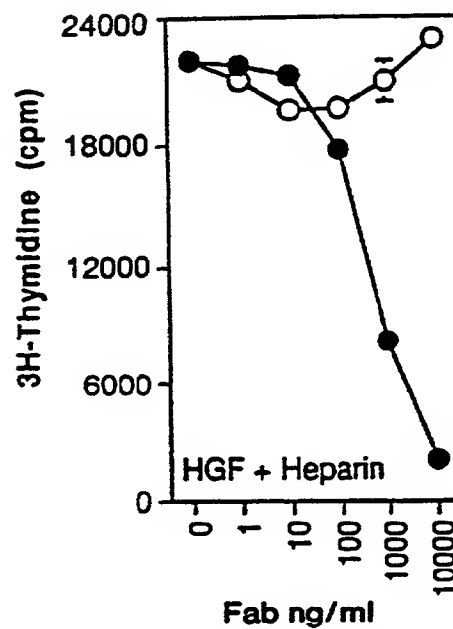


FIG. 14D